Balanced transcription of cell division genes in Bacillus subtilis as revealed by single cell analysis

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Figure S1. Defining cell-cycle progression and exponential length growth in *Bacillus subtilis*

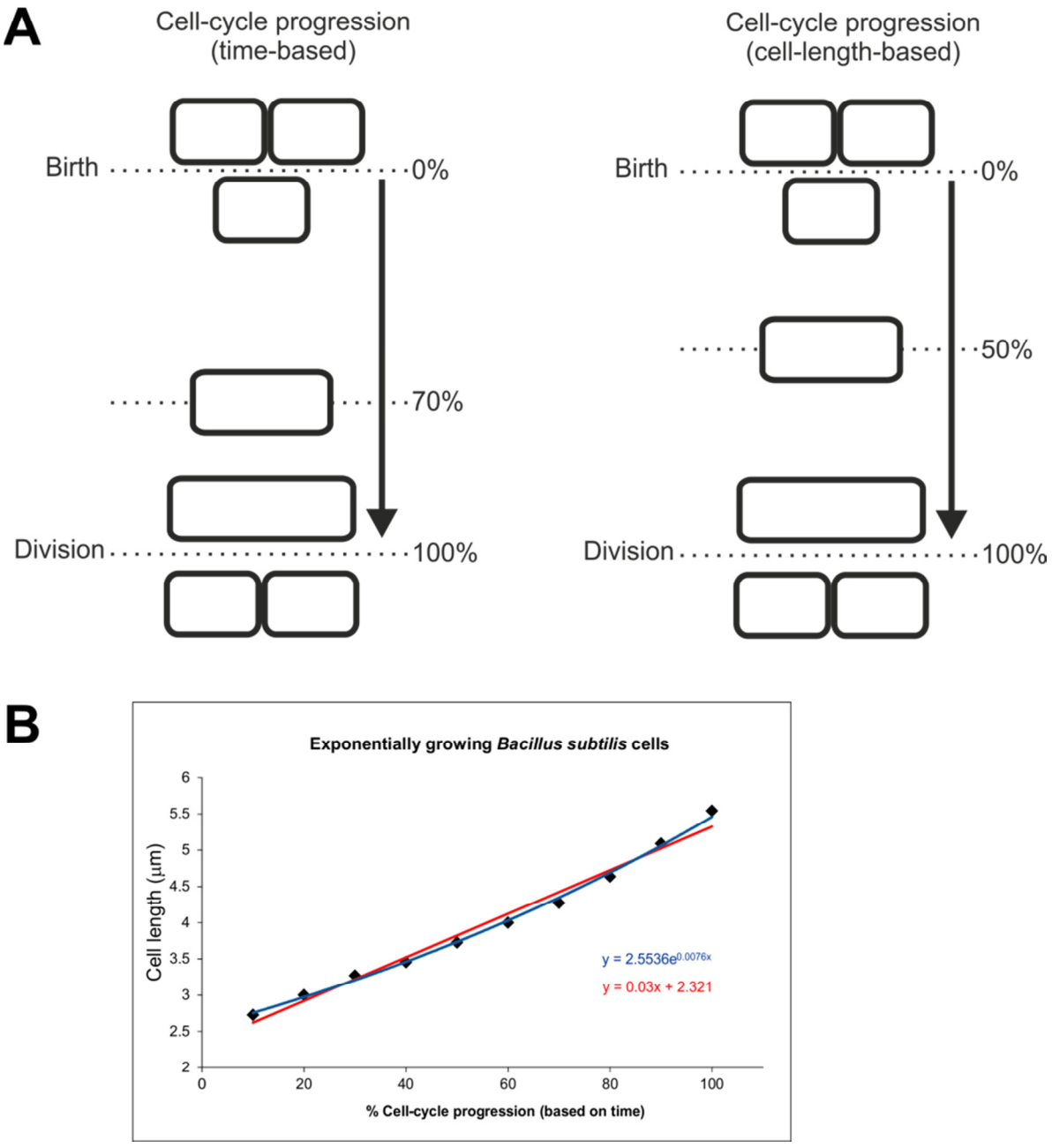

Fig. S1. Defining cell-cycle progression and exponential length growth.

A. Cell-cycle progression defined as a function of time since birth and new cell division (left). Cell-cycle progression defined as a function of cell length (% of maximal cell length at time prior to new cell division) (right).

B. More than 900 data points of exponentially growing *B. subtilis* cells are plotted as a function of the cell-cycle progression in time (see *Experimental procedures*). The data points are much a better fit to an exponential curve than to a line ($R^2 = 0.997$ versus 0.982 respectively),

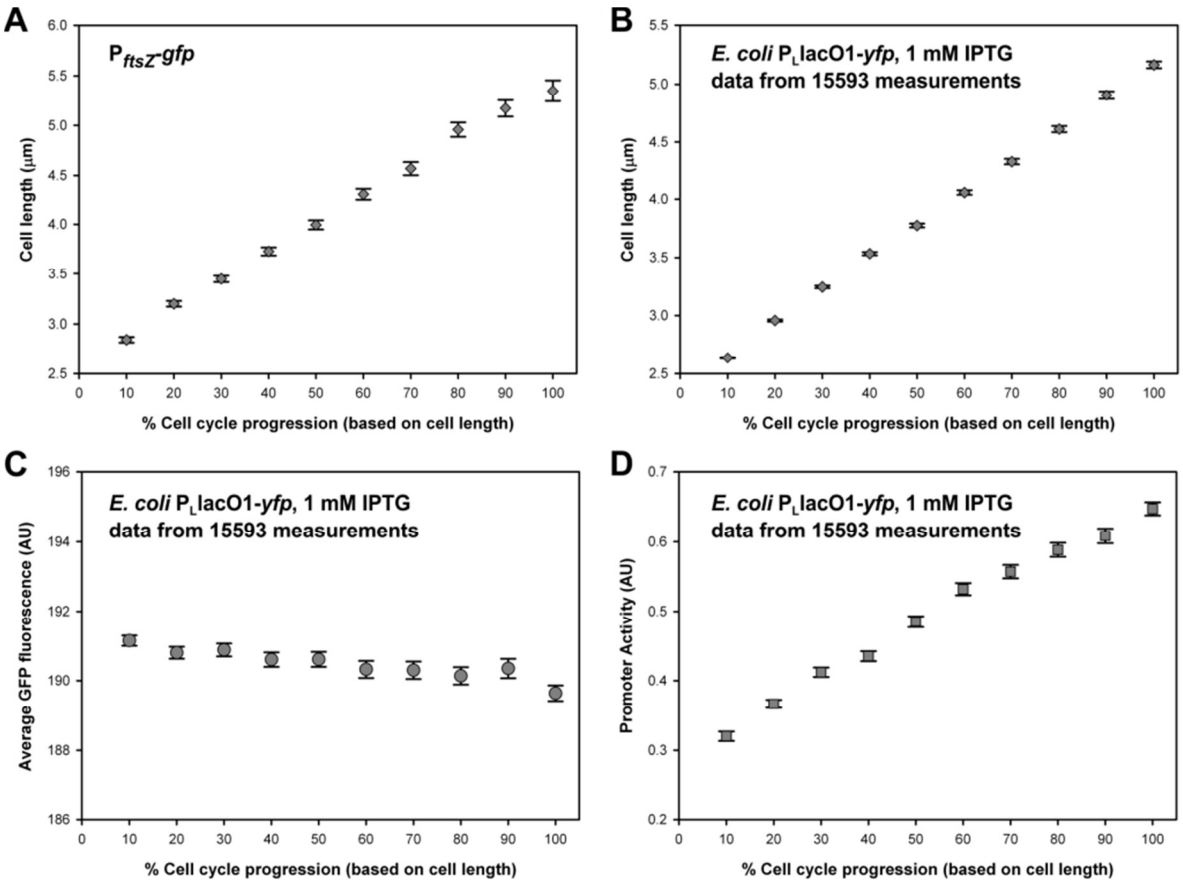

Fig. S2. Validation of our cell-cycle progression software routines.

A. All data points of *B. subtilis* P*ftsZ–gfp* (~ 900) were plotted as a function of cell-cycle progression based on cell length versus cell length. A clear straight line is visible demonstrating that the binning procedure works as expected. Error bars represent standard error of the mean.

B. Same as for (A) but now on a large (15593 data points) *E. coli* data set (Stewart *et al*., 2005).

C. Average fluorescence from cells carrying an IPTG inducible YFP construct grown in the presence of 1 mM IPTG as a function of cell-cycle progression. Same data set as used for (B). Error bars indicate standard error of the mean.

D. Promoter activity (normalized GFP production per minute) as a function of cell-cycle progression for the *E. coli* data set. Error bars indicate standard error of the mean. Note the approximate twofold increase in PA at the end of the cell cycle.

Movie S1. This film shows approximately 20 h of the growth of a *B. subtilis* microcolony harbouring the P*ftsZ–gfp* construct. Images were taken every 8 min. Scale bar: 10 μm.